

<110> Andrew D. MURDIN, Raymond P. OOMEN, Joe WANG, Pamela DUNN

<130> 77813-9

<140>

<141>

<150> US 60/123,966

<151> 1999-03-12

<160> 4

<170> PatentIn Ver. 2.0

<210> 1

$\langle 211 \rangle$ 2111

<212> DNA

<213> Chlamydia pneumoniae

<220>

<221> CDS

<222> (139) .. (1809)

<400> 1

ttgatcaggt agttaggaga tgaattraatt cctgactacc ttaattcaga taataaaccc 60

aaatgttgag ggtaagagtt tacaaaacat tctacccgat ggcagaagaa aaaaataaac 120

atgcgatagg agatccct atg tcc aaa ctc atc aga cga gta gtt acg gtc 171
Met Ser Lys Leu Ile Arg Arg Val Val Thr Val
1 5 10

ctt gcg cta acg agt atg gcg agt tgc ttt gcc agc ggg ggt ata gag 219
Leu Ala Leu Thr Ser Met Ala Ser Cys Phe Ala Ser Gly Gly Ile Glu
 15 20 25

gcc gct gta gca gag tct ctg att act aag atc gtc gct agt gcg gaa 267
Ala Ala Val Ala Glu Ser Leu Ile Thr Lys Ile Val Ala Ser Ala Glu
30 35 40

aca aag cca gca cct gtt / cct atg aca gcg aag aag gtt aga ctt gtc 315
Thr Lys Pro Ala Pro Val / Pro Met Thr Ala Lys Lys Val Arg Leu Val
45 50 55

cgt aga aat aaa caa / cca gtt gaa caa aaa agc cgt ggt gct ttt tgt 363
 Arg Arg Asn Lys Gln Pro Val Glu Gln Lys Ser Arg Gly Ala Phe Cys
 60 65 70 75

gat aaa gaa ttt tat ccc tgt gaa gag gga cga tgt caa cct gta gag 411
Asp Lys Glu Phe Tyr Pro Cys Glu Glu Gly Arg Cys Gln Pro Val Glu
80 85 90

gct cag caa gag tct tgc tac gga aga ttg tat tct gta aaa gta aac 459
 Ala Gln Gln Glu Ser Cys Tyr Gly Arg Leu Tyr Ser Val Lys Val Asn
 95 100 105

gat gat tgc aac gta gaa att tgc cag tcc gtt cca gaa tac gct act 507
 Asp Asp Cys Asn Val Glu Ile Cys Gln Ser Val Pro Glu Tyr Ala Thr
 110 115 120

gta gga tct cct tac cct att gaa atc ctt gct ata ggc aaa aaa gat 555
 Val Gly Ser Pro Tyr Pro Ile Glu Ile Leu Ala Ile Gly Lys Lys Asp
 125 130 135

tgt gtt gat gtt gtg att aca caa cag cta cct tgc gaa gct gaa ttc 603
 Cys Val Asp Val Val Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe
 140 145 150 155

gta agc agt gat cca gaa aca act cct aca agt gat ggg aaa tta gtc 651
 Val Ser Ser Asp Pro Glu Thr Thr Pro Thr Ser Asp Gly Lys Leu Val
 160 165 170

tgg aaa atc gat cgc ctg ggt gca gga gat aaa tgc aaa att act gta 699
 Trp Lys Ile Asp Arg Leu Gly Ala Gly Asp Lys Cys Lys Ile Thr Val
 175 180 185

tgg gta aaa cct ctt aaa gaa ggt tgc tgc ttc aca gct gct act gta 747
 Trp Val Lys Pro Leu Lys Glu Gly Cys Cys Phe Thr Ala Ala Thr Val
 190 195 200

tgt gct tgc cca gag ctc cgt tct tat act aaa tgc ggt caa cca gcc 795
 Cys Ala Cys Pro Glu Leu Arg Ser Tyr Thr Lys Cys Gly Gln Pro Ala
 205 210 215

att tgt att aag caa gaa gga cct gac tgt gct tgc cta aga tgc cct 843
 Ile Cys Ile Lys Gln Glu Gly Pro Asp Cys Ala Cys Leu Arg Cys Pro
 220 225 230 235

gta tgc tac aaa atc gaa gta gtg aac aca gga tct gct att gcc cgt 891
 Val Cys Tyr Lys Ile Glu Val Val Asn Thr Gly Ser Ala Ile Ala Arg
 240 245 250

aac gta act gta gat aat cct gtt ccc gat ggc tat tct cat gca tct 939
 Asn Val Thr Val Asp Asn Pro Val Pro Asp Gly Tyr Ser His Ala Ser
 255 260 265

ggt caa aga gtt ctc tct ttt aac tta gga gac atg aga cct ggc gat 987
 Gly Gln Arg Val Leu Ser Phe Asn Leu Gly Asp Met Arg Pro Gly Asp
 270 275 280

aaa aag gta ttt aca gtt gag ttc tgc cct caa aga aga ggt caa atc 1035
 Lys Lys Val Phe Thr Val Glu Phe Cys Pro Gln Arg Arg Gly Gln Ile
 285 290 295

act aac gtt gct act gta act tac tgc ggt gga cac aaa tgt tct gca 1083
 Thr Asn Val Ala Thr Val Thr Tyr Cys Gly Gly His Lys Cys Ser Ala
 300 305 310 315

gcgccggatc cgatacacgt gggatatttc tgtg 34